SEQUENCE LISTING

<110> JENTSCH, Thomas J.

<120> NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS

<130> 2815-127P

<140>
<141>

<160> 41

<170> PatentIn Ver. 2.1

<210> 1
<211> 2335
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (1)..(2335)

<220>
<221> CDS
<222> (33)..(2170)

<400> 1
agccatgcgt ctctgagcgc cccgagcgcg ccccccgccc ggaccgtgcc cgggccccgg 60

cgccccagc cgggcgccgc cc atg gcc gag gcc ccc ccg cgc cgc ctc ggc 112
Met Ala Glu Ala Pro Pro Arg Arg Leu Gly
1 5 10

ctg ggc ccc ccg ccc ggg gac gcc ccc cgc gcg gag cta gtg gcg ctc 160
Leu Gly Pro Pro Pro Gly Asp Ala Pro Arg Ala Glu Leu Val Ala Leu
15 20 25

acg gcc gtg cag agc gaa cag ggc gag gcg ggc ggg ggc ggc tcc ccg 208
Thr Ala Val Gln Ser Glu Gln Gly Glu Ala Gly Gly Gly Gly Ser Pro
30 35 40

cgc cgc ctc ggc ctc ctg ggc agc ccc ctg ccg ccg ggc gcg ccc ctc 256
Arg Arg Leu Gly Leu Leu Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu
45 50 55

[illegible] 304
Pro Gly Pro Gly Ser Gly Ser Gly Ser Ala Cys Gly Gln Arg Ser Ser
60 65 70

gcc gcg cac aag cgc tac cgc cgc ctg cag aac tgg gtc tac aac gtg 352
Ala Ala His Lys Arg Tyr Arg Arg Leu Gln Asn Trp Val Tyr Asn Val
75 80 85 90

ctg gag cgg ccc cgc ggc tgg gcc ttc gtc tac cac gtc ttc ata ttt 400
Leu Glu Arg Pro Arg Gly Trp Ala Phe Val Tyr His Val Phe Ile Phe
95 100 105

ttg ctg gtc ttc agc tgc ctg gtg ctg tct gtg ctg tcc act atc cag 448
Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Leu Ser Thr Ile Gln
110 115 120

gag cac cag gaa ctt gcc aac gag tgt ctc ctc atc ttg gaa ttc gtg 496
Glu His Gln Glu Leu Ala Asn Glu Cys Leu Leu Ile Leu Glu Phe Val
125 130 135

atg atc gtg gtt ttc ggc ttg gag tac atc gtc cgg gtc tgg tcc gcc 544
Met Ile Val Val Phe Gly Leu Glu Tyr Ile Val Arg Val Trp Ser Ala
140 145 150

gga tgc tgc tgc cgc tac cga gga tgg cag ggt cgc ttc cgc ttt gcc 592
Gly Cys Cys Cys Arg Tyr Arg Gly Trp Gln Gly Arg Phe Arg Phe Ala
155 160 165 170

aga aag ccc ttc tgt gtc atc gac ttc atc gtg ttc gtg gcc tcg gtg 640
Arg Lys Pro Phe Cys Val Ile Asp Phe Ile Val Phe Val Ala Ser Val
175 180 185

gcc gtc atc gcc gcg ggt acc cag ggc aac atc ttc gcc acg tcc gcg 688
Ala Val Ile Ala Ala Gly Thr Gln Gly Asn Ile Phe Ala Thr Ser Ala
190 195 200

ctg cgc agc atg cgc ttc ctg cag atc ctg cgc atg gtg cgc atg gac 736
Leu Arg Ser Met Arg Phe Leu Gln Ile Leu Arg Met Val Arg Met Asp
205 210 215

cgc cgc ggc ggc acc tgg aag ctg ctg ggc tca gtg gtc tac gcg cat 784
Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val Val Tyr Ala His
220 225 230

agc aag gag ctg atc acc gcc tgg tac atc ggg ttc ctg gtg ctc atc 832
Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile
235 240 245 250

```
... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ...  ...
... Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Asp Ala Asn Ser Asp
                255                 260                 265

ttc tcc tcc tac gcc gac tcg ctc tgg tgg ggg acg att aca ttg aca  928
Phe Ser Ser Tyr Ala Asp Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr
            270                 275                 280

acc atc ggc tat ggt gac aag aca ccg cac aca tgg ctg ggc agg gtc  976
Thr Ile Gly Tyr Gly Asp Lys Thr Pro His Thr Trp Leu Gly Arg Val
        285                 290                 295

ctg gct gct ggc ttc gcc tta ctg ggc atc tct ttc ttt gcc ctg cct 1024
Leu Ala Ala Gly Phe Ala Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro
    300                 305                 310

gcc ggc atc cta ggc tcc ggc ttt gcc ctg aag gtc cag gag cag cac 1072
Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val Gln Glu Gln His
315                 320                 325                 330

cgg cag aag cac ttc gag aag cgg agg atg ccg gca gcc aac ctc atc 1120
Arg Gln Lys His Phe Glu Lys Arg Arg Met Pro Ala Ala Asn Leu Ile
                335                 340                 345

cag gct gcc tgg cgc ctg tac tcc acc gat atg agc cgg gcc tac ctg 1168
Gln Ala Ala Trp Arg Leu Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu
            350                 355                 360

aca gcc acc tgg tac tac tat gac agt atc ctc cca tcc ttc aga gag 1216
Thr Ala Thr Trp Tyr Tyr Tyr Asp Ser Ile Leu Pro Ser Phe Arg Glu
        365                 370                 375

ctg gcc ctc ttg ttt gag cac gtg caa cgg gcc cgc aat ggg ggc cta 1264
Leu Ala Leu Leu Phe Glu His Val Gln Arg Ala Arg Asn Gly Gly Leu
    380                 385                 390

cgg ccc ctg gag gtg cgg cgg gcg ccg gta ccc gac gga gca ccc tcc 1312
Arg Pro Leu Glu Val Arg Arg Ala Pro Val Pro Asp Gly Ala Pro Ser
395                 400                 405                 410

cgt tac ccg ccc gtt gcc acc tgc cac cgg ccg ggc agc acc tcc ttc 1360
Arg Tyr Pro Pro Val Ala Thr Cys His Arg Pro Gly Ser Thr Ser Phe
                415                 420                 425

tgc cct ggg gaa agc agc cgg atg ggc atc aaa gac cgc atc cgc atg 1408
Cys Pro Gly Glu Ser Ser Arg Met Gly Ile Lys Asp Arg Ile Arg Met
            430                 435                 440
```

[illegible] 1456
Gly Ser Ser Gln Arg Arg Thr Gly Pro Ser Lys Gln Gln Leu Ala Pro
445 450 455

cca aca atg ccc acc tcc cca agc agc gag cag gtg ggt gag gcc acc 1504
Pro Thr Met Pro Thr Ser Pro Ser Ser Glu Gln Val Gly Glu Ala Thr
460 465 470

agc ccc acc aag gtg caa aag agc tgg agc ttc aat gac cgc acc cgc 1552
Ser Pro Thr Lys Val Gln Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg
475 480 485 490

ttc cgg gca tct ctg aga ctc aaa ccc cgc acc tct gct gag gat gcc 1600
Phe Arg Ala Ser Leu Arg Leu Lys Pro Arg Thr Ser Ala Glu Asp Ala
495 500 505

ccc tca gag gaa gta gca gag gag aag agc tac cag tgt gag ctc acg 1648
Pro Ser Glu Glu Val Ala Glu Glu Lys Ser Tyr Gln Cys Glu Leu Thr
510 515 520

gtg gac gac atc atg cct gct gtg aag aca gtc atc cgc tcc atc agg 1696
Val Asp Asp Ile Met Pro Ala Val Lys Thr Val Ile Arg Ser Ile Arg
525 530 535

att ctc aag ttc ctg gtg gcc aaa agg aaa ttc aag gag aca ctg cga 1744
Ile Leu Lys Phe Leu Val Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg
540 545 550

ccg tac gac gtg aag gac gtc att gag cag tac tca gca ggc cac ctg 1792
Pro Tyr Asp Val Lys Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu
555 560 565 570

gac atg ctg ggc cgg atc aag agc ctg caa act cgg gtg gac caa att 1840
Asp Met Leu Gly Arg Ile Lys Ser Leu Gln Thr Arg Val Asp Gln Ile
575 580 585

gtg ggt cgg ggg ccc ggg gac agg aag gcc cgg gag aag ggc gac aag 1888
Val Gly Arg Gly Pro Gly Asp Arg Lys Ala Arg Glu Lys Gly Asp Lys
590 595 600

ggg ccc tcc gac gcg gag gtg gtg gat gaa atc agc atg atg gga cgc 1936
Gly Pro Ser Asp Ala Glu Val Val Asp Glu Ile Ser Met Met Gly Arg
605 610 615

gtg gtc aag gtg gag aag cag gtg cag tcc atc gag cac aag ctg gac 1984
Val Val Lys Val Glu Lys Gln Val Gln Ser Ile Glu His Lys Leu Asp
620 625 630

[illegible]

Leu Leu Leu Gly Phe Tyr Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala
635 640 645 650

agc ctg ggc gcc gtg caa gtg ccg ctg ttc gac ccc gac atc acc tcc 2080
Ser Leu Gly Ala Val Gln Val Pro Leu Phe Asp Pro Asp Ile Thr Ser
655 660 665

gac tac cac agc cct gtg gac cac gag gac atc tcc gtc tcc gca cag 2128
Asp Tyr His Ser Pro Val Asp His Glu Asp Ile Ser Val Ser Ala Gln
670 675 680

acg ctc agc atc tcc cgc tcg gtc agc acc aac atg gac tga 2170
Thr Leu Ser Ile Ser Arg Ser Val Ser Thr Asn Met Asp
685 690 695

gggacttctc agaggcaggg cagcacacgg ccagccccgc ggcctggcgc tccgactgcc 2230

ctctgaggcc tccggactcc tctcgtactt gaactcactc cctcacgggg agagagacca 2290

cacgcagtat tgagctgcct gagtgggcgt ggtacctgct gtggg 2335

<210> 2
<211> 695
<212> PRT
<213> Homo sapiens

<400> 2
Met Ala Glu Ala Pro Pro Arg Arg Leu Gly Leu Gly Pro Pro Pro Gly
1 5 10 15
Asp Ala Pro Arg Ala Glu Leu Val Ala Leu Thr Ala Val Gln Ser Glu
20 25 30
Gln Gly Glu Ala Gly Gly Gly Gly Ser Pro Arg Arg Leu Gly Leu Leu
35 40 45
Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu Pro Gly Pro Gly Ser Gly
50 55 60
Ser Gly Ser Ala Cys Gly Gln Arg Ser Ser Ala Ala His Lys Arg Tyr
65 70 75 80
Arg Arg Leu Gln Asn Trp Val Tyr Asn Val Leu Glu Arg Pro Arg Gly
85 90 95
Trp Ala Phe Val Tyr His Val Phe Ile Phe Leu Leu Val Phe Ser Cys
100 105 110
Leu Val Leu Ser Val Leu Ser Thr Ile Gln Glu His Gln Glu Leu Ala
115 120 125
Asn Glu Cys Leu Leu Ile Leu Glu Phe Val Met Ile Val Val Phe Gly
130 135 140
Leu Glu Tyr Ile Val Arg Val Trp Ser Ala Gly Cys Cys Cys Arg Tyr

Arg Gly Trp Gln Gly Arg Phe Arg Phe Ala Arg Lys Pro Phe Cys Val
165 170 175
Ile Asp Phe Ile Val Phe Val Ala Ser Val Ala Val Ile Ala Ala Gly
180 185 190
Thr Gln Gly Asn Ile Phe Ala Thr Ser Ala Leu Arg Ser Met Arg Phe
195 200 205
Leu Gln Ile Leu Arg Met Val Arg Met Asp Arg Arg Gly Gly Thr Trp
210 215 220
Lys Leu Leu Gly Ser Val Val Tyr Ala His Ser Lys Glu Leu Ile Thr
225 230 235 240
Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile Phe Ala Ser Phe Leu Val
245 250 255
Tyr Leu Ala Glu Lys Asp Ala Asn Ser Asp Phe Ser Ser Tyr Ala Asp
260 265 270
Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp
275 280 285
Lys Thr Pro His Thr Trp Leu Gly Arg Val Leu Ala Ala Gly Phe Ala
290 295 300
Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser
305 310 315 320
Gly Phe Ala Leu Lys Val Gln Glu Gln His Arg Gln Lys His Phe Glu
325 330 335
Lys Arg Arg Met Pro Ala Ala Asn Leu Ile Gln Ala Ala Trp Arg Leu
340 345 350
Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu Thr Ala Thr Trp Tyr Tyr
355 360 365
Tyr Asp Ser Ile Leu Pro Ser Phe Arg Glu Leu Ala Leu Leu Phe Glu
370 375 380
His Val Gln Arg Ala Arg Asn Gly Gly Leu Arg Pro Leu Glu Val Arg
385 390 395 400
Arg Ala Pro Val Pro Asp Gly Ala Pro Ser Arg Tyr Pro Pro Val Ala
405 410 415
Thr Cys His Arg Pro Gly Ser Thr Ser Phe Cys Pro Gly Glu Ser Ser
420 425 430
Arg Met Gly Ile Lys Asp Arg Ile Arg Met Gly Ser Ser Gln Arg Arg
435 440 445
Thr Gly Pro Ser Lys Gln Gln Leu Ala Pro Pro Thr Met Pro Thr Ser
450 455 460
Pro Ser Ser Glu Gln Val Gly Glu Ala Thr Ser Pro Thr Lys Val Gln
465 470 475 480
Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg Phe Arg Ala Ser Leu Arg
485 490 495
Leu Lys Pro Arg Thr Ser Ala Glu Asp Ala Pro Ser Glu Glu Val Ala
500 505 510
Glu Glu Lys Ser Tyr Gln Cys Glu Leu Thr Val Asp Asp Ile Met Pro
515 520 525
Ala Val Lys Thr Val Ile Arg Ser Ile Arg Ile Leu Lys Phe Leu Val

Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys Asp
545 550 555 560
Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Gly Arg Ile
565 570 575
Lys Ser Leu Gln Thr Arg Val Asp Gln Ile Val Gly Arg Gly Pro Gly
580 585 590
Asp Arg Lys Ala Arg Glu Lys Gly Asp Lys Gly Pro Ser Asp Ala Glu
595 600 605
Val Val Asp Glu Ile Ser Met Met Gly Arg Val Val Lys Val Glu Lys
610 615 620
Gln Val Gln Ser Ile Glu His Lys Leu Asp Leu Leu Leu Gly Phe Tyr
625 630 635 640
Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala Ser Leu Gly Ala Val Gln
645 650 655
Val Pro Leu Phe Asp Pro Asp Ile Thr Ser Asp Tyr His Ser Pro Val
660 665 670
Asp His Glu Asp Ile Ser Val Ser Ala Gln Thr Leu Ser Ile Ser Arg
675 680 685
Ser Val Ser Thr Asn Met Asp
690 695

<210> 3
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 3
catgrgtctc tgagcgcccc gagc 24

<210> 4
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 4
aggccaggct tgcgcgggga aacg 24

<210> 5
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 5
[illegible]cagag ctgaac[illegible] agg 23

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 6
aagctgctct ctgagccatg g 21

<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 7
[illegible]ggtccg cgctgtgacc 20

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 8
[illegible]gtctccagg gtcagagtcg 20

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 9
[illegible] 21

<210> 10
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 10
gagacagccc ctctgacctc g 21

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 11
atcgcctttcc cgtgtggaag c 21

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 12
agtcacgatg ggcagacctc g 21

<200> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 13
[illegible] 21

<210> 14
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 14
atgtgtcaca ggggtgagc 19

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 15
[illegible]atgggg acacccttgc 20

<210> 16
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 16
gcacagggtt gacacacc 18

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 17
atttggagta accacaactg g 21

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 18
gctcccctgg gagccatcac c 21

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 19
tttatctagg agctctgtgc 20

<210> 20
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 20
accacgaaag tggctgaagg c 21

<400> 21
[illegible] agctttgtcc 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 22
cctcagacgg ccctcgatcg 20

<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 23
[illegible]tg gtggtttggc 20

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 24
ctcctgacct caagtgatcc 20

<200>
<211>
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 25
[illegible] 21

<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 26
aactcagctg cagcagtgag c 21

<210> 27
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 27
[illegible] 21

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 28
aacgcatcct cccatgtca 20

<2110>
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 29
[illegible] 23

<210> 30
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 30
catgaggaag tgagttcaag tacg 24

<210> 31
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 31
attactgat ggagcgccct ctcg 24

<210> 32
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 32
tcatccaccg taagctcaca ctgg 24

<213> Homo sapiens

<400> 33

Met Ala Ala Ala Ser Ser Pro Pro Arg Ala Glu Arg Lys Arg Trp Gly
1 5 10 15

Trp Gly Arg Leu Pro Gly Ala Arg Arg Gly Ser Ala Gly Leu Ala Lys
20 25 30

Lys Cys Pro Phe Ser Leu Glu Leu Ala Glu Gly Gly Pro Ala Gly Gly
35 40 45

Ala Leu Tyr Ala Pro Ile Ala Pro Gly Ala Pro Gly Pro Ala Pro Pro
50 55 60

Ala Ser Pro Ala Ala Pro Ala Ala Pro Pro Val Ala Ser Asp Leu Gly
65 70 75 80

Pro Arg Pro Pro Val Ser Leu Asp Pro Arg Val Ser Ile Tyr Ser Thr
85 90 95

Arg Arg Pro Val Leu Ala Arg Thr His Val Gln Gly Arg Val Tyr Asn
100 105 110

Phe Leu Glu Arg Pro Thr Gly Trp Lys Cys Phe Val Tyr His Phe Ala
115 120 125

Val Phe Leu Ile Val Leu Val Cys Leu Ile Phe Ser Val Leu Ser Thr
130 135 140

Ile Glu Gln Tyr Ala Ala Leu Ala Thr Gly Thr Leu Phe Trp Met Glu
145 150 155 160

Ile Val Leu Val Val Phe Phe Gly Thr Glu Tyr Val Val Arg Leu Trp
165 170 175

Ser Ala Gly Cys Arg Ser Lys Tyr Val Gly Leu Trp Gly Arg Leu Arg
180 185 190

Phe Ala Arg Lys Pro Ile Ser Ile Ile Asp Leu Ile Val Val Val Ala
195 200 205

Ser Met Val Val Leu Cys Val Gly Ser Lys Gly Gln Val Phe Ala Thr
210 215 220

Asp Ala Ile Arg Gly Ile Arg Ile Leu Met Tyr Leu Arg Met Leu His
225 230 235 240

Val Asp Arg Gln Gly Gly Thr Trp Arg Leu Leu Gly Ser Val Val Phe
245 250 255

Ile His Arg Gln Glu Leu Ile Thr Thr Leu Tyr Ile Gly Phe Leu Gly
260 265 270

Leu Ile Phe Ser Ser Tyr Phe Val Tyr Leu Ala Glu Lys Asp Ala Val
275 280 285

Asn Glu Ser Gly Arg Val Glu Phe Gly Ser Tyr Ala Asp Ala Leu Trp
290 295 300

Trp Gly Val Val Thr Val Thr Thr Ile Gly Tyr Gly Asp Lys Val Pro
305 310 315 320

Gln Thr Trp Val Gly Lys Thr Ile Ala Ser Cys Phe Ser Val Phe Ala
325 330 335

Ile Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala
340 345 350

Leu Lys Val Gln Gln Lys Gln Arg Gln Lys His Phe Asn Arg Gln Ile
355 360 365

Pro Ala Ala Ala Ser Leu Ile Gln Thr Ala Trp Arg Cys Tyr Ala Ala
370 375 380

Glu Asn Pro Asp Ser Ser Thr Trp Lys Ile Tyr Ile Arg Lys Ala Pro
385 390 395 400

Arg Ser His Thr Leu Leu Ser Pro Ser Pro Lys Pro Lys Lys Ser Val
405 410 415

Val Val Lys Lys Lys Lys Phe Lys Leu Asp Lys Asp Asn Gly Val Thr
420 425 430

Pro Gly Glu Lys Met Leu Thr Val Pro His Ile Thr Cys Asp Pro Pro
435 440 445

Glu Glu Arg Arg Leu Asp His Phe Ser Val Asp Gly Tyr Asp Ser Ser
450 455 460

Val Arg Lys Ser Pro Thr Leu Leu Glu Val Ser Met Pro His Phe Met
465 470 475 480

Arg Thr Asn Ser Ile Ala Phe Asp Ile Asp Leu Glu Gly Glu Thr Leu
485 490 495

Leu Thr Pro Ile Thr His Ile Ser Gln Leu Arg Glu His His Arg Ala
500 505 510

Thr Ile Lys Val Ile Arg Arg Met Gln Tyr Phe Val Ala Lys Lys Lys
515 520 525

Phe Gln Gln Ala Arg Lys Pro Tyr Asp Val Arg Asp Val Ile Glu Gln
530 535 540

Tyr Ser Gln Gly His Leu Asn Leu Met Val Arg Ile Lys Glu Leu Gln
545 550 555 560

Arg Arg Leu Asp Gln Ser Ile Gly Lys Pro Ser Leu Phe Ile Ser Val
565 570 575

Ser Glu Lys Ser Lys Asp Arg Gly Ser Asn Thr Ile Gly Ala Arg Leu
580 585 590

Asn Arg Val Glu Asp Lys Val Thr Gln Leu Asp Gln Arg Leu Ala Leu
595 600 605

Ile Thr Asp Met Leu His Gln Leu Leu Ser Leu His Gly Gly Ser Thr
610 615 620

Pro Gly Ser Gly Gly Pro Pro Arg Glu Gly Gly Ala His Ile Thr Gln
625 630 635 640

Pro Cys Gly Ser Gly Gly Ser Val Asp Pro Glu Leu Phe Leu Pro Ser
645 650 655

Asn Thr Leu Pro Thr Tyr Glu Gln Leu Thr Val Pro Arg Arg Gly Pro
660 665 670

Asp Glu Gly Ser
675

<210> 34
<211> 844
<212> PRT
<213> Homo sapiens

<400> 34
Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly
1 5 10 15

Xaa Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
20 25 30

Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
35 40 45

Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
50 55 60

Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
65 70 75 80

Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
85 90 95

Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
100 105 110

Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
115 120 125

Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
130 135 140

Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
145 150 155 160

Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
165 170 175

Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
180 185 190

Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
195 200 205

Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
210 215 220

Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
225 230 235 240

Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
245 250 255

Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
260 265 270

Val Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
275 280 285

Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
290 295 300

Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
305 310 315 320

Gln Gln Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
325 330 335

Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
340 345 350

Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
355 360 365

Val Pro Met Tyr Arg Leu Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu
370 375 380

Arg Asn Leu Lys Ser Lys Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro
385 390 395 400

Pro Glu Pro Ser Pro Ser Gln Lys Val Ser Leu Lys Asp Arg Val Phe
405 410 415

Ser Ser Pro Arg Gly Val Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala
420 425 430

Gln Thr Val Arg Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser
435 440 445

Pro Ser Lys Val Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala
450 455 460

Arg Gln Ala Phe Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu
465 470 475 480

Glu Ala Ser Leu Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro
485 490 495

Cys Glu Phe Val Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile
500 505 510

Arg Ala Val Cys Val Met Arg Phe Leu Val Ser Lys Arg Lys Phe Lys
515 520 525

Xaa Ser Leu Arg Pro Tyr Asp Val Met Asp Val Ile Glu Gln Tyr Ser
530 535 540

Ala Gly His Leu Asp Met Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg
545 550 555 560

Val Asp Gln Ile Val Gly Arg Gly Pro Ala Ile Thr Asp Lys Asp Arg
565 570 575

Thr Lys Gly Pro Ala Glu Ala Glu Leu Pro Glu Asp Pro Ser Met Met
580 585 590

Gly Arg Leu Gly Lys Val Glu Lys Gln Val Leu Ser Met Glu Lys Lys
595 600 605

Leu Asp Phe Leu Val Asn Ile Tyr Met Gln Arg Met Gly Ile Pro Pro
610 615 620

Thr Glu Thr Glu Ala Tyr Phe Gly Ala Lys Glu Pro Glu Pro Ala Pro
625 630 635 640

Pro Tyr His Ser Pro Glu Asp Ser Arg Glu His Val Asp Arg His Gly
645 650 655

Cys Ile Val Lys Ile Val Arg Ser Ser Ser Ser Thr Gly Gln Lys Asn
660 665 670

Phe Ser Ala Pro Pro Ala Ala Pro Pro Val Gln Cys Pro Pro Ser Thr
675 680 685

Ser Trp Gln Pro Gln Ser His Pro Arg Gln Gly His Gly Thr Ser Pro
690 695 700

Val Gly Asp His Gly Ser Leu Val Arg Ile Pro Pro Pro Pro Ala His
705 710 715 720

Glu Arg Ser Leu Ser Ala Tyr Gly Gly Gly Asn Arg Ala Ser Met Glu
725 730 735

Phe Leu Arg Gln Glu Asp Thr Pro Gly Cys Arg Pro Pro Glu Gly Thr
740 745 750

Leu Arg Asp Ser Asp Thr Ser Ile Ser Ile Pro Ser Val Asp His Glu
755 760 765

Glu Leu Gln Arg Ser Phe Ser Gly Phe Ser Ile Ser Gln Ser Lys Glu
770 775 780

Asn Leu Asp Ala Leu Asn Ser Cys Tyr Ala Ala Val Ala Pro Cys Ala
785 790 795 800

Lys Val Arg Pro Tyr Ile Ala Glu Gly Glu Ser Asp Thr Asp Ser Asp
805 810 815

Leu Cys Thr Pro Cys Gly Pro Pro Pro Arg Ser Ala Thr Gly Glu Gly
820 825 830

Pro Phe Gly Asp Val Gly Trp Ala Gly Pro Arg Lys
835 840

<210> 35
<211> 872
<212> PRT
<213> Homo sapiens

<400> 35
Met Gly Leu Lys Ala Arg Arg Ala Ala Gly Ala Ala Gly Gly Gly Gly
1 5 10 15

Asp Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala Asn Pro Ala Gly Gly Asp
20 25 30

Ala Ala Ala Ala Gly Asp Glu Glu Arg Lys Val Gly Leu Ala Pro Gly
35 40 45

Asp Val Glu Gln Val Thr Leu Ala Leu Gly Ala Gly Ala Asp Lys Asp
50 55 60

Gly Thr Leu Leu Leu Glu Gly Gly Gly Arg Asp Glu Gly Gln Arg Arg
65 70 75 80

Thr Pro Gln Gly Ile Gly Leu Leu Ala Lys Thr Pro Leu Ser Arg Pro
85 90 95

Val Lys Arg Asn Asn Ala Lys Tyr Arg Arg Ile Gln Thr Leu Ile Tyr
100 105 110

Asp Ala Leu Glu Arg Pro Arg Gly Trp Ala Leu Leu Tyr His Ala Leu
115 120 125

Val Phe Leu Ile Val Leu Gly Cys Leu Ile Leu Ala Val Leu Thr Thr
130 135 140

Phe Lys Glu Tyr Glu Thr Val Ser Gly Asp Trp Leu Leu Leu Leu Glu

Thr Phe Ala Ile Phe Ile Phe Gly Ala Glu Phe Ala Leu Arg Ile Trp
165 170 175

Ala Ala Gly Cys Cys Cys Arg Tyr Lys Gly Trp Arg Gly Arg Leu Lys
180 185 190

Phe Ala Arg Lys Pro Leu Cys Met Leu Asp Ile Phe Val Leu Ile Ala
195 200 205

Ser Val Pro Val Val Ala Val Gly Asn Gln Gly Asn Val Leu Ala Thr
210 215 220

Ser Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met Leu Arg Met
225 230 235 240

Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Ala Ile Cys Ala
245 250 255

His Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu Thr Leu
260 265 270

Ile Leu Ser Ser Phe Leu Val Tyr Leu Val Glu Lys Asp Val Pro Glu
275 280 285

Val Asp Ala Gln Gly Glu Glu Met Lys Glu Glu Phe Glu Thr Tyr Ala
290 295 300

Asp Ala Leu Trp Trp Gly Leu Ile Thr Leu Ala Thr Ile Gly Tyr Gly
305 310 315 320

Asp Lys Thr Pro Lys Thr Trp Glu Gly Arg Leu Ile Ala Ala Thr Phe
325 330 335

Ser Leu Ile Gly Val Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly
340 345 350

Ser Gly Leu Ala Leu Lys Val Gln Glu Gln His Arg Gln Lys His Phe
355 360 365

Glu Lys Arg Arg Lys Pro Ala Ala Glu Leu Ile Gln Ala Ala Trp Arg
370 375 380

Tyr Tyr Ala Thr Asn Pro Asn Arg Ile Asp Leu Val Ala Thr Trp Arg
385 390 395 400

Phe Tyr Glu Ser Val Val Ser Phe Pro Phe Phe Arg Lys Glu Gln Leu

Glu Ala Ala Ser Ser Gln Lys Leu Gly Leu Leu Asp Arg Val Arg Leu
420 425 430

Ser Asn Pro Arg Gly Ser Asn Thr Lys Gly Lys Leu Phe Thr Pro Leu
435 440 445

Asn Val Asp Ala Ile Glu Glu Ser Pro Ser Lys Glu Pro Lys Pro Val
450 455 460

Gly Leu Asn Asn Lys Glu Arg Phe Arg Thr Ala Phe Arg Met Lys Ala
465 470 475 480

Tyr Ala Phe Trp Gln Ser Ser Glu Asp Ala Gly Thr Gly Asp Pro Met
485 490 495

Ala Glu Asp Arg Gly Tyr Gly Asn Asp Phe Pro Ile Glu Asp Met Ile
500 505 510

Pro Thr Leu Lys Ala Ala Ile Arg Ala Val Arg Ile Leu Gln Phe Arg
515 520 525

Leu Tyr Lys Lys Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys
530 535 540

Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Ser Arg
545 550 555 560

Ile Lys Tyr Leu Gln Thr Arg Ile Asp Met Ile Phe Thr Pro Gly Pro
565 570 575

Pro Ser Thr Pro Lys His Lys Lys Ser Gln Lys Gly Ser Ala Phe Thr
580 585 590

Phe Pro Ser Gln Gln Ser Pro Arg Asn Glu Pro Tyr Val Ala Arg Pro
595 600 605

Ser Thr Ser Glu Ile Glu Asp Gln Ser Met Met Gly Lys Phe Val Lys
610 615 620

Val Glu Arg Gln Val Gln Asp Met Gly Lys Lys Leu Asp Phe Leu Val
625 630 635 640

Asp Met His Met Gln His Met Glu Arg Leu Gln Val Gln Val Thr Glu
645 650 655

Tyr Tyr Pro Thr Lys Gly Thr Ser Ser Pro Ala Glu Ala Glu Lys Lys

Glu Asp Asn Arg Tyr Ser Asp Leu Lys Thr Ile Ile Cys Asn Tyr Ser
675 680 685

Glu Thr Gly Pro Pro Glu Pro Pro Tyr Ser Phe His Gln Val Thr Ile
690 695 700

Asp Lys Val Ser Pro Tyr Gly Phe Phe Ala His Asp Pro Val Asn Leu
705 710 715 720

Pro Arg Gly Gly Pro Ser Ser Gly Lys Val Gln Ala Thr Pro Pro Ser
725 730 735

Ser Ala Thr Thr Tyr Val Glu Arg Pro Thr Val Leu Pro Ile Leu Thr
740 745 750

Leu Leu Asp Ser Arg Val Ser Cys His Ser Gln Ala Asp Leu Gln Gly
755 760 765

Pro Tyr Ser Asp Arg Ile Ser Pro Arg Gln Arg Arg Ser Ile Thr Arg
770 775 780

Asp Ser Asp Thr Pro Leu Ser Leu Met Ser Val Asn His Glu Glu Leu
785 790 795 800

Glu Arg Ser Pro Ser Gly Phe Ser Ile Ser Gln Asp Arg Asp Asp Tyr
805 810 815

Val Phe Gly Pro Asn Gly Gly Ser Ser Trp Met Arg Glu Lys Arg Tyr
820 825 830

Leu Ala Glu Gly Glu Thr Asp Thr Asp Thr Asp Pro Phe Thr Pro Ser
835 840 845

Gly Ser Met Pro Leu Ser Ser Thr Gly Asp Gly Ile Ser Asp Ser Val
850 855 860

Trp Thr Pro Ser Asn Lys Pro Ile
865 870

<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

Description of Artificial Sequence: PCR Primer

aaggctggat cagtccattg g 21

210> 37
211> 21
212> DNA
213> Artificial Sequence

220>
223> Description of Artificial Sequence: PCR Primer

400> 37
gcgrggacag gctgttgctg g 21

210> 38
211> 21
212> DNA
213> Artificial Sequence

220>
223> Description of Artificial Sequence: PCR Primer

400> 38
gccagccac ctccccgtg g 21

210> 39
211> 23
212> DNA
213> Artificial Sequence

220>
223> Description of Artificial Sequence: PCR Primer

400> 39
ctctctgcaa tgtagggcct gac 23

210> 40
211> 24
212> DNA
213> Artificial Sequence

220>

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 41
cagaagagtc aagatgggca ggac 24